

**AMENDMENTS TO THE CLAIMS**

1-18. (Canceled)

19. (Currently Amended) A method of identifying a protein fold comprising determining the distribution of amino acid residues in different thermodynamic environments corresponding to a known protein structure, wherein said distribution of amino acid residues identifies a protein fold in a protein;

20. (Original) The method of claim 19, wherein the thermodynamic environments are selected from the group consisting of stability, enthalpy and entropy.

21. (Original) The method of claim 19, wherein determining the distribution of amino acid residues comprises constructing scoring matrices derived of thermodynamic information.

22. (Original) The method of claim 21, wherein the scoring matrices are derived from COREX stability, enthalpy or entropy information.

23-33. (Canceled)

34. (Original) A computer-readable medium having computer-executable instructions for performing the steps recited in claim 19.

35. (Original) A computer-readable medium having computer-executable instructions for performing the steps recited in claim 22.

36-38. (Canceled)